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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/965,313

DATE: 10/18/2001
TIME: 16:18:36

Input Set : A:\Sequencing Listing as filed.txt
Output Set: N:\CRF3\10182001\I965313.raw

ENTERED

2 .

4 <110> APPLICANT: Hodge, Martin R.
6 <120> TITLE OF INVENTION: Novel IL-9/IL-2 Receptor-Like Molecules
7 and Uses Thereof
9 <130> FILE REFERENCE: 5800-17A
C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/965,313
C--> 11 <141> CURRENT FILING DATE: 2001-09-26
11 <150> PRIOR APPLICATION NUMBER: US 09/313,913
12 <151> PRIOR FILING DATE: 1999-05-18
14 <160> NUMBER OF SEQ ID NOS: 8
16 <170> SOFTWARE: FastSEQ for Windows Version 3.0
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19 <211> LENGTH: 2343
20 <212> TYPE: DNA
21 <213> ORGANISM: Homo sapiens
23 <220> FEATURE:
24 <221> NAME/KEY: CDS
25 <222> LOCATION: (349)...(1962)
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29 cgcctggta cttccttgc gcctcttcc tctgtctgtc gctctgtgg acacctgcct 120
30 ggaggccca agtggccgtca tcagagtgc acgtcttatg acagcctgtat tggtgactcg 180
31 ggctgggtgt ggattctcac cccaggcctc tgccctgttt ctcagacccat catctgtcac 240
32 ccccacgctg aaccaggctg ccaccccccag aagccccatca gactgcccccc agcacacgg 300
33 atggatttct gagaagaaga agggccgtgg gagtcagc atg ccg cgt 357
34 Met Pro Arg
35 1
37 ggc tgg gcc ccc ctg ctc ctg ctg ctc cag gga ggc tgg ggc 405
38 Gly Trp Ala Ala Pro Leu Leu Leu Leu Leu Gln Gly Gly Trp Gly
39 5 10 15
41 tgc ccc gac ctc gtc tgc tac acc gat tac ctc cag acg gtc atc tgc 453
42 Cys Pro Asp Leu Val Cys Tyr Thr Asp Tyr Leu Gln Thr Val Ile Cys
43 20 25 30 35
45 atc ctg gaa atg tgg aac ctc cac ccc acg ctc acc ctt acc tgg 501
46 Ile Leu Glu Met Trp Asn Leu His Pro Ser Thr Leu Thr Leu Thr Trp
47 40 45 50
49 caa gac cag tat gaa gag ctg aag gac gag gcc acc tcc tgc agc ctc 549
50 Gln Asp Gln Tyr Glu Glu Leu Lys Asp Glu Ala Thr Ser Cys Ser Leu
51 55 60 65
53 cac agg tcg gcc cac aat gcc acg cat gcc acc tac acc tgc cac atg 597
54 His Arg Ser Ala His Asn Ala Thr His Ala Thr Tyr Thr Cys His Met
55 70 75 80
57 gat gta ttc cac ttc atg gcc gac gac att ttc agt gtc aac atc aca 645
58 Asp Val Phe His Met Ala Asp Asp Ile Phe Ser Val Asn Ile Thr
59 85 90 95
61 gac cag tct ggc aac tac tcc cag gag tgt ggc agc ttt ctc ctg gct 693
62 Asp Gln Ser Gly Asn Tyr Ser Gln Glu Cys Gly Ser Phe Leu Leu Ala
63 100 105 110 115

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65	gag agc atc aag ccg gct ccc cct ttc aac gtg act gtg acc ttc tca	741
66	Glu Ser Ile Lys Pro Ala Pro Pro Phe Asn Val Thr Val Thr Phe Ser	
67	120 125 130	
69	gga cag tat aat atc tcc tgg cgc tca gat tac gaa gac cct gcc ttc	789
70	Gly Gln Tyr Asn Ile Ser Trp Arg Ser Asp Tyr Glu Asp Pro Ala Phe	
71	135 140 145	
73	tac atg ctg aag ggc aag ctt cag tat gag ctg cag tac agg aac cgg	837
74	Tyr Met Leu Lys Gly Lys Leu Gln Tyr Glu Leu Gln Tyr Arg Asn Arg	
75	150 155 160	
77	gga gac ccc tgg gct gtg agt ccg agg aga aag ctg atc tca gtg gac	885
78	Gly Asp Pro Trp Ala Val Ser Pro Arg Arg Lys Leu Ile Ser Val Asp	
79	165 170 175	
81	tca aga agt gtc tcc ctc ccc ctg gag ttc cgc aaa gac tcg agc	933
82	Ser Arg Ser Val Ser Leu Leu Pro Leu Glu Phe Arg Lys Asp Ser Ser	
83	180 185 190 195	
85	tat gag ctg cag gtg cgg gca ggg ccc atg cct ggc tcc tcc tac cag	981
86	Tyr Glu Leu Gln Val Arg Ala Gly Pro Met Pro Gly Ser Ser Tyr Gln	
87	200 205 210	
89	ggg acc tgg agt gaa tgg agt gac ccg gtc atc ttt cag acc cag tca	1029
90	Gly Thr Trp Ser Glu Trp Ser Asp Pro Val Ile Phe Gln Thr Gln Ser	
91	215 220 225	
93	gag gag tta aag gaa ggc tgg aac cct cac ctg ctg ctt ctc ctc ctg	1077
94	Glu Glu Leu Lys Glu Gly Trp Asn Pro His Leu Leu Leu Leu Leu	
95	230 235 240	
97	ctt gtc ata gtc ttc att cct gcc ttc tgg agc ctg aag acc cat cca	1125
98	Leu Val Ile Val Phe Ile Pro Ala Phe Trp Ser Leu Lys Thr His Pro	
99	245 250 255	
101	ttg tgg agg cta tgg aag aag ata tgg gcc gtc ccc agc cct gag cgg	1173
102	Leu Trp Arg Leu Trp Lys Lys Ile Trp Ala Val Pro Ser Pro Glu Arg	
103	260 265 270 275	
105	ttc ttc atg ccc ctg tac aag ggc tgc agc gga gac ttc aag aaa tgg	1221
106	Phe Phe Met Pro Leu Tyr Lys Gly Cys Ser Gly Asp Phe Lys Lys Trp	
107	280 285 290	
109	gtg ggt gca ccc ttc act ggc tcc agc ctg gag ctg gga ccc tgg agc	1269
110	Val Gly Ala Pro Phe Thr Gly Ser Ser Leu Glu Leu Gly Pro Trp Ser	
111	295 300 305	
113	cca gag gtg ccc tcc acc ctg gag gtg tac agc tgc cac cca cca cgg	1317
114	Pro Glu Val Pro Ser Thr Leu Glu Val Tyr Ser Cys His Pro Pro Arg	
115	310 315 320	
117	agc ccg gcc aag agg ctg cag ctc acg gag cta caa gaa cca gca gag	1365
118	Ser Pro Ala Lys Arg Leu Gln Leu Thr Glu Leu Gln Glu Pro Ala Glu	
119	325 330 335	
121	ctg gtg gag tct gac ggt gtg ccc aag ccc agc ttc tgg ccg aca gcc	1413
122	Leu Val Glu Ser Asp Gly Val Pro Lys Pro Ser Phe Trp Pro Thr Ala	
123	340 345 350 355	
125	cag aac tcg ggg ggc tca gct tac agt gag gag agg gat cgg cca tac	1461
126	Gln Asn Ser Gly Gly Ser Ala Tyr Ser Glu Glu Arg Asp Arg Pro Tyr	
127	360 365 370	
129	ggc ctg gtg tcc att gac aca gtg act gtg cta gat gca gag ggg cca	1509

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130	Gly Leu Val Ser Ile Asp Thr Val Thr Val Leu Asp Ala Glu Gly Pro			
131	375	380	385	
133	tgc acc tgg ccc tgc agc tgt gag gat gac ggc tac cca gcc ctg gac			1557
134	Cys Thr Trp Pro Cys Ser Cys Glu Asp Asp Gly Tyr Pro Ala Leu Asp			
135	390	395	400	
137	ctg gat gct ggc ctg gag ccc agc cca ggc cta gag gac cca ctc ttg			1605
138	Leu Asp Ala Gly Leu Glu Pro Ser Pro Gly Leu Glu Asp Pro Leu Leu			
139	405	410	415	
141	gat gca ggg acc aca gtc ctg tcc tgt ggc tgt gtc tca gct ggc agc			1653
142	Asp Ala Gly Thr Thr Val Leu Ser Cys Gly Cys Val Ser Ala Gly Ser			
143	420	425	430	435
145	cct ggg cta gga ggg ccc ctg gga agc ctc ctg gac aga cta aag cca			1701
146	Pro Gly Leu Gly Pro Leu Gly Ser Leu Leu Asp Arg Leu Lys Pro			
147	440	445	450	
149	ccc ctt gca gat ggg gag gac tgg gct ggg gga ctg ccc tgg ggt ggc			1749
150	Pro Leu Ala Asp Gly Glu Asp Trp Ala Gly Gly Leu Pro Trp Gly Gly			
151	455	460	465	
153	cgg tca cct gga ggg gtc tca gag agt gag gcg ggc tca ccc ctg gcc			1797
154	Arg Ser Pro Gly Gly Val Ser Glu Ser Glu Ala Gly Ser Pro Leu Ala			
155	470	475	480	
157	ggc ctg gat atg gac acg ttt gac agt ggc ttt gtg ggc tct gac tgc			1845
158	Gly Leu Asp Met Asp Thr Phe Asp Ser Gly Phe Val Gly Ser Asp Cys			
159	485	490	495	
161	agc agc cct gtg gag tgt gac ttc acc agc ccc ggg gac gaa gga ccc			1893
162	Ser Ser Pro Val Glu Cys Asp Phe Thr Ser Pro Gly Asp Glu Gly Pro			
163	500	505	510	515
165	ccc cgg agc tac ctc cgc cag tgg gtg gtc att cct ccg cca ctt tcg			1941
166	Pro Arg Ser Tyr Leu Arg Gln Trp Val Val Ile Pro Pro Pro Leu Ser			
167	520	525	530	
169	agc cct gga ccc cag gcc agc taatgaggct gactggatgt ccagagctgg			1992
170	Ser Pro Gly Pro Gln Ala Ser			
171	535			
173	ccagggccact ggccctgag ccagagacaa ggtcacctgg gctgtatgt gaagacacct			2052
174	gcagcccttg gtcctctgga tggccctttg agcctgtatgt ttacagtgtc ttttgtgtgt			2112
175	tgtcatatg ttttgtgtgt catatgtatg ttttgtgtgt ttttgtgtctt agtgtgcgcag			2172
176	tggcatgtcc acgtgtgtgt gtgattgcac gtgcctgtgg gcctggata atgccccatgg			2232
177	tactccatgc attcacctgc cctgtcatatg ttttgtgtca cggagctcac ccatgtgcac			2292
178	aagtgtgcac agtaaacgtg ttttgtgtca aaaaaaaaaaaaaaaa aaaaaaaaaa a			2343
180	<210> SEQ ID NO: 2			
181	<211> LENGTH: 538			
182	<212> TYPE: PRT			
183	<213> ORGANISM: Homo sapiens IL-2/IL-9 Receptor Like			
185	<400> SEQUENCE: 2			
186	Met Pro Arg Gly Trp Ala Ala Pro Leu Leu Leu Leu Leu Gln Gly			
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188	Gly Trp Gly Cys Pro Asp Leu Val Cys Tyr Thr Asp Tyr Leu Gln Thr			
189	20	25	30	
190	Val Ile Cys Ile Leu Glu Met Trp Asn Leu His Pro Ser Thr Leu Thr			
191	35	40	45	

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192 Leu Thr Trp Gln Asp Gln Tyr Glu Glu Leu Lys Asp Glu Ala Thr Ser
193      50          55          60
194 Cys Ser Leu His Arg Ser Ala His Asn Ala Thr His Ala Thr Tyr Thr
195      65          70          75          80
196 Cys His Met Asp Val Phe His Phe Met Ala Asp Asp Ile Phe Ser Val
197      85          90          95
198 Asn Ile Thr Asp Gln Ser Gly Asn Tyr Ser Gln Glu Cys Gly Ser Phe
199      100         105         110
200 Leu Leu Ala Glu Ser Ile Lys Pro Ala Pro Pro Phe Asn Val Thr Val
201      115         120         125
202 Thr Phe Ser Gly Gln Tyr Asn Ile Ser Trp Arg Ser Asp Tyr Glu Asp
203      130         135         140
204 Pro Ala Phe Tyr Met Leu Lys Gly Lys Leu Gln Tyr Glu Leu Gln Tyr
205      145         150         155         160
206 Arg Asn Arg Gly Asp Pro Trp Ala Val Ser Pro Arg Arg Lys Leu Ile
207      165         170         175
208 Ser Val Asp Ser Arg Ser Val Ser Leu Leu Pro Leu Glu Phe Arg Lys
209      180         185         190
210 Asp Ser Ser Tyr Glu Leu Gln Val Arg Ala Gly Pro Met Pro Gly Ser
211      195         200         205
212 Ser Tyr Gln Gly Thr Trp Ser Glu Trp Ser Asp Pro Val Ile Phe Gln
213      210         215         220
214 Thr Gln Ser Glu Glu Leu Lys Glu Gly Trp Asn Pro His Leu Leu Leu
215      225         230         235         240
216 Leu Leu Leu Leu Val Ile Val Phe Ile Pro Ala Phe Trp Ser Leu Lys
217      245         250         255
218 Thr His Pro Leu Trp Arg Leu Trp Lys Lys Ile Trp Ala Val Pro Ser
219      260         265         270
220 Pro Glu Arg Phe Phe Met Pro Leu Tyr Lys Gly Cys Ser Gly Asp Phe
221      275         280         285
222 Lys Lys Trp Val Gly Ala Pro Phe Thr Gly Ser Ser Leu Glu Leu Gly
223      290         295         300
224 Pro Trp Ser Pro Glu Val Pro Ser Thr Leu Glu Val Tyr Ser Cys His
225      305         310         315         320
226 Pro Pro Arg Ser Pro Ala Lys Arg Leu Gln Leu Thr Glu Leu Gln Glu
227      325         330         335
228 Pro Ala Glu Leu Val Glu Ser Asp Gly Val Pro Lys Pro Ser Phe Trp
229      340         345         350
230 Pro Thr Ala Gln Asn Ser Gly Gly Ser Ala Tyr Ser Glu Glu Arg Asp
231      355         360         365
232 Arg Pro Tyr Gly Leu Val Ser Ile Asp Thr Val Thr Val Leu Asp Ala
233      370         375         380
234 Glu Gly Pro Cys Thr Trp Pro Cys Ser Cys Glu Asp Asp Gly Tyr Pro
235      385         390         395         400
236 Ala Leu Asp Leu Asp Ala Gly Leu Glu Pro Ser Pro Gly Leu Glu Asp
237      405         410         415
238 Pro Leu Leu Asp Ala Gly Thr Thr Val Leu Ser Cys Gly Cys Val Ser
239      420         425         430
240 Ala Gly Ser Pro Gly Leu Gly Pro Leu Gly Ser Leu Leu Asp Arg

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```

241      435          440          445
242 Leu Lys Pro Pro Leu Ala Asp Gly Glu Asp Trp Ala Gly Gly Leu Pro
243      450          455          460
244 Trp Gly Gly Arg Ser Pro Gly Gly Val Ser Glu Ser Gly Ala Gly Ser
245      465          470          475          480
246 Pro Leu Ala Gly Leu Asp Met Asp Thr Phe Asp Ser Gly Phe Val Gly
247      485          490          495
248 Ser Asp Cys Ser Ser Pro Val Glu Cys Asp Phe Thr Ser Pro Gly Asp
249      500          505          510
250 Glu Gly Pro Pro Arg Ser Tyr Leu Arg Gln Trp Val Val Ile Pro Pro
251      515          520          525
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253      530          535
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256 <211> LENGTH: 2456
257 <212> TYPE: DNA
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260 <220> FEATURE:
261 <221> NAME/KEY: CDS
262 <222> LOCATION: (391)...(1977)
264 <400> SEQUENCE: 3
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266 gtctgccat ccctggggca gccaactggc ctcagccccgt gccccaggcg tgccctgtct 120
267 ctgtctggct gccccagccc tactgtcttc ctctgtgttag gctctgccc gatgccccggc 180
268 tggtcctcag cctcaggact atctcagcag tgactccccc gattctggac ttgcacctga 240
269 ctgaacctct gcccacctca aaccttcacc tcccaccc accactccga gtccccgtgt 300
270 gactcccacg cccaggagac cacccaaagtg ccccaagcta aagaatggct ttctgaggaa 360
271 gatcctgaag gagtaggtct gggacacagc atg ccc cgg ggc cca gtg gct gcc 414
272                               Met Pro Arg Gly Pro Val Ala Ala
273                               1           5
275 tta ctc ctg ctg att ctc cat gga gct tgg agc tgc ctg gac ctc act 462
276 Leu Leu Leu Ile Leu His Gly Ala Trp Ser Cys Leu Asp Leu Thr
277      10          15          20
279 tgc tac act gac tac ctc tgg acc atc acc tgt gtc ctg gag aca cgg 510
280 Cys Tyr Thr Asp Tyr Leu Trp Thr Ile Thr Cys Val Leu Glu Thr Arg
281      25          30          35          40
283 agc ccc aac ccc agc ata ctc agt ctc acc tgg caa gat gaa tat gag 558
284 Ser Pro Asn Pro Ser Ile Leu Ser Leu Thr Trp Gln Asp Glu Tyr Glu
285      45          50          55
287 gaa ctt cag gac caa gag acc ttc tgc agc cta cac aag tct ggc cac 606
288 Glu Leu Gln Asp Gln Glu Thr Phe Cys Ser Leu His Lys Ser Gly His
289      60          65          70
291 aac acc aca cat ata tgg tac acg tgc cat atg cgc ttg tct caa ttc 654
292 Asn Thr Thr His Ile Trp Tyr Thr Cys His Met Arg Leu Ser Gln Phe
293      75          80          85
295 ctg tcc gat gaa gtt ttc att gtc aac gtg acg gac cag tct ggc aac 702
296 Leu Ser Asp Glu Val Phe Ile Val Asn Val Thr Asp Gln Ser Gly Asn
297      90          95          100
299 aac tcc caa gag tgt ggc agc ttt gtc ctg gct gag agc atc aag cca 750

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VERIFICATION SUMMARY

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DATE: 10/18/2001

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Input Set : A:\Sequencing Listing as filed.txt
Output Set: N:\CRF3\10182001\I965313.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application No
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date